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<120> ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR

<130> 3492-WO

<140> --to be assigned--
 <141> 2004-11-04

<150> 60/518,166
 <151> 2003-11-07

<160> 77

<170> PatentIn version 3.2

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 <212> DNA
 <213> Homo sapien

<220>

<221> CDS
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ctg ctg cag gtg gca agc tct ggg aac atg aag gtc ttg cag gag ccc	96
Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro	
20 25 30	
acc tgc gtc tcc gac tac atg agc atc tct act tgc gag tgg aag atg	144
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met	
35 40 45	
aat ggt ccc acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg	192
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu	
50 55 60	
gtt ttt ctg ctc tcc gaa gcc cac acg tgt atc cct gag aac aac gga	240
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly	
65 70 75 80	
ggc gcg ggg tgc gtg tgc cac ctg ctc atg gat gac gtg gtc agt gcg	288
Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala	
85 90 95	
gat aac tat aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag	336
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys	
100 105 110	

ggc tcc ttc aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac	384
Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn	
115 120 125	
ctg aca gtt cac acc aat gtc tcc gac act ctg ctg ctg acc tgg agc	432
Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Thr Trp Ser	
130 135 140	
aac ccg tat ccc cct gac aat tac ctg tat aat cat ctc acc tat gca	480
Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala	
145 150 155 160	
gtc aac att tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac	528
Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn	
165 170 175	
gtg acc tac cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag	576
Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys	
180 185 190	
tct ggg att tcc tac agg gca cgg gtg agg gcc tgg gct cag tgc tat	624
Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr	
195 200 205	
aac acc acc tgg agt gag tgg agc ccc agc acc aag tgg cac aac tcc	672
Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser	
210 215 220	
tac agg gag ccc ttc gag cag cac ctc ctg ctg ggc gtc agc gtt tcc	720
Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser	
225 230 235 240	
tgc att gtc atc ctc gcc gtc tgc ctg ttg tgc tat gtc agc atc acc	768
Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr	
245 250 255	
aag att aag aaa gaa tgg tgg gat cag att ccc aac cca gcc cgc agc	816
Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser	
260 265 270	
cgc ctc gtg gct ata ata atc cag gat gct cag ggg tca cag tgg gag	864
Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu	
275 280 285	
aag cgg tcc cga ggc cag gaa cca gcc aag tgc cca cac tgg aag aat	912
Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn	
290 295 300	
tgt ctt acc aag ctc ttg ccc tgt ttt ctg gag cac aac atg aaa agg	960
Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg	
305 310 315 320	
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Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser	
325 330 335	
gga aaa tca gca tgg tgc cca gtg gag atc agc aag aca gtc ctc tgg	1056
Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp	
340 345 350	

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Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro			
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Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu			
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ggc att gtg gcc cgg cta aca gag agc ctg ttc ctg gac ctg ctc gga		1248	
Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly			
405	410	415	
gag gag aat ggg ggc ttt tgc cag cag gac atg ggg gag tca tgc ctt		1296	
Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu			
420	425	430	
ctt cca cct tcg gga agt acg agt gct cac atg ccc tgg gat gag ttc		1344	
Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe			
435	440	445	
cca agt gca ggg ccc aag gag gca cct ccc tgg ggc aag gag cag cct		1392	
Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro			
450	455	460	
ctc cac ctg gag cca agt cct cct gcc agc ccg acc cag agt cca gac		1440	
Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp			
465	470	475	480
aac ctg act tgc aca gag acg ccc ctc gtc atc gca ggc aac cct gct		1488	
Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala			
485	490	495	
tac cgc agc ttc agc aac tcc ctg agc cag tca ccg tgt ccc aga gag		1536	
Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu			
500	505	510	
ctg ggt cca gac cca ctg ctg gcc aga cac ctg gag gaa gta gaa ccc		1584	
Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Val Glu Pro			
515	520	525	
gag atg ccc tgt gtc ccc cag ctc tct gag cca acc act gtg ccc caa		1632	
Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln			
530	535	540	
cct gag cca gaa acc tgg gag cag atc ctc cgc cga aat gtc ctc cag		1680	
Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln			
545	550	555	560
cat ggg gca gct gca gcc ccc gtc tcg gcc ccc acc agt ggc tat cag		1728	
His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln			
565	570	575	
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Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val			
580	585	590	

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tgc cct ggg gac cct gcc cca gtc cct gtc ccc ttg ttc acc ttt gga Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly 645 650 655	1968
ctg gac agg gag cca cct cgc agt ccg cag agc tca cat ctc cca agc Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser 660 665 670	2016
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atg cca aag ccc cca ctt ccc cag gag cag gac gcc aca gac ccc ctt gtg Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val 690 695 700	2112
gac agc ctg ggc agt ggc att gtc tac tca gcc ctt acc tgc cac ctg Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu 705 710 715 720	2160
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cct gtc atg gcc agt cct tgc tgt ggc tgc tgc tgt gga gac agg tcc Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Gly Asp Arg Ser 740 745 750	2256
tcg ccc cct aca acc ccc ctg agg gcc cca gac ccc tct cca ggt ggg Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly 755 760 765	2304
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atc tca gag aag agt aaa tcc tca tca tcc ttc cat cct gcc cct ggc Ile Ser Glu Lys Ser Lys Ser Ser Ser Phe His Pro Ala Pro Gly 785 790 795 800	2400
aat gct cag agc tca agc cag acc ccc aaa atc gtg aac ttt gtc tcc Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser 805 810 815	2448
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<213> Homo sapien

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Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
35 40 45

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
50 55 60

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
65 70 75 80

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
85 90 95

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
100 105 110

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
115 120 125

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
130 135 140

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
145 150 155 160

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
165 170 175

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
180 185 190

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr
195 200 205

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
210 215 220

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser
225 230 235 240

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr
245 250 255

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser
260 265 270

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu
275 280 285

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn
290 295 300

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg
305 310 315 320

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser
325 330 335

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp
340 345 350

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro
355 360 365

Val Glu Cys Glu Glu Glu Glu Val Glu Glu Lys Gly Ser Phe
370 375 380

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu
385 390 395 400

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly
405 410 415

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu
420 425 430

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe
435 440 445

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro
450 455 460

Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp
465 470 475 480

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala
485 490 495

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu
500 505 510

Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro
515 520 525

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln
530 535 540

Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln
545 550 555 560

His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln
565 570 575

Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val
580 585 590

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser
595 600 605

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala
610 615 620

Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly
625 630 635 640

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly
645 650 655

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser
660 665 670

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp
675 680 685

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val
690 695 700

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu
 705 710 715 720

Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr
 725 730 735

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser
 740 745 750

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly
 755 760 765

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly
 770 775 780

Ile Ser Glu Lys Ser Lys Ser Ser Ser Phe His Pro Ala Pro Gly
 785 790 795 800

Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser
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Val Gly Pro Thr Tyr Met Arg Val Ser
 820 825

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 <213> Artificial

<220>
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<220>
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc ttt ggt gca tcc agc agg ggc act ggc atc cca gac agg ttc agt 192
 Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agg aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<220>
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc aac agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser	
20 25 30	

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

atc tat ggt gca tcc agc agg gcc cct ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gat cac tca gca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala	
85 90 95	

ggg tgg acg ttc ggc caa ggg acc aag gtg gag atc aaa	327
Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

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<223> Synthetic Construct

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20 25 30	

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala
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Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag act gtt aac agc gac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Asn Ser Asp
 20 25 30

tac tta gcc tgg tac cag cag aaa ccg ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtc tat tac tgt cag cag tat ggt agg tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aaa gtg gat atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
 100 105

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 <212> PRT
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<220>

<223> Synthetic Construct

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	20				25						30				

Tyr	Leu	Ala	Trp	Tyr	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35				40						45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50				55					60					

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65				70					75				80		

Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Arg	Ser	Pro
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<222> (1)..(327)

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1			5						10					15		

gaa	aga	gcc	acc	ctc	tcc	tgc	agg	gcc	agt	cag	agt	gtt	agc	agc	gac	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asp	
	20				25							30				

tac	tta	gcc	tgg	tac	cag	cag	aaa	cct	ggc	cag	gct	ccc	agg	ctc	ctc	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	
	35				40						45					

atc tat ggt gca tct agc agg gcc tct ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg ttt ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<400> 11

gat att gtg ctg acc cag tct cca gcc acc ctg tct ttg tct cca ggg	48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt aac agc aac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

atc tat ggt aca tcc tac agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

ggc agt ggg tct ggg aca gac ttc act ctc acc atc acc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu	
65 70 75 80	

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	

ccg tgg acg ttc ggc caa ggg aca cga ctg gag att aaa	327
Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys	
100 105	

<210> 12

<211> 109

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 12

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 13

<211> 327

<212> DNA

<213> Artificial

<220>

<223> Light chain variable sequence

<220>

<221> CDS

<222> (1)...(327)

<400> 13

gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg 48
 Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 20 25 30

tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa 327
 Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 14

<211> 109

<212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 14

Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 15
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 15
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 16
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
115

<210> 17
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 17

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca
Val Ser Ser
115 345

<210> 18
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 19
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1) .. (345)

<400> 19
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 20
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 20

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 21
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 21 48
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 22
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 23

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)...(345)

<400> 23

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 24
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 24

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 25
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 25

gag	gtt	cag	ttg	gtg	cag	tct	ggg	gga	ggc	ttg	gta	cat	cct	ggg	ggg	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Gly	
1							5			10				15		

tcc	ctg	aga	ctc	tcc	tgt	gca	ggc	tct	gga	ttc	acc	ttc	agt	aga	aat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn	
								20		25			30			

gct	atg	ttc	tgg	gtt	cgc	cag	gct	cca	gga	aaa	ggt	ctg	gag	tgg	gta	144
Ala	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
							35			40		45				

tca	ggt	att	ggt	act	ggt	ggt	gcc	aca	aac	tat	gca	gac	tcc	gtg	aag	192
Ser	Gly	Ile	Gly	Thr	Gly	Gly	Ala	Thr	Asn	Tyr	Ala	Asp	Ser	Val	Lys	
							50			55		60				

ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	gcc	aag	aac	tcc	ttg	tat	ctt	240
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	
							65			70		75		80		

caa	atg	aac	agc	ctg	aga	gcc	gag	gac	atg	gct	gtg	tat	tac	tgt	gca	288
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Met	Ala	Val	Tyr	Tyr	Cys	Ala	
							85			90			95			

aga	ggg	agg	tac	tgg	tac	ccg	tgg	tgg	ggc	cag	gga	acc	ctg	gtc	acc	336
Arg	Gly	Arg	Tyr	Trp	Tyr	Pro	Trp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
							100			105			110			

gtc	tcc	tca														345
Val	Ser	Ser														
		115														

<210>	26															
<211>	115															
<212>	PRT															
<213>	Artificial															

<220>																
<223>	Synthetic	Construct														

<400>	26															
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Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Leu	Val	His	Pro	Gly	Gly	
1							5			10			15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn
								20		25			30		

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 27
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 27
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 28
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 29
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 29
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 30
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 30
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 31
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 31
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 .5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca
Val Ser Ser
115

345

<210> 32
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct
<400> 32

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 33
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)...(345)

<400> 33
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 34
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 35
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 35
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 36
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 36

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 37
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 37

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	
<210> 38	
<211> 115	
<212> PRT	
<213> Artificial	
<220>	
<223> Synthetic Construct	
<400> 38	
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 39
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 39
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca
 Val Ser Ser
 115

<210> 40
 <211> 115

<212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 40

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 41
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 41
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
35 40 45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	192
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	240
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr, Tyr Cys Ala	288
85 90 95	
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	336
100 105 110	
gtc tcc tca Val Ser Ser	345
115	

<210> 42
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct
<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 43
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 43
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 44
 <211> 115
 <212> PRT
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 44

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1															
							5				10			15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn
							20			25			30		

Ala	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
							35		40			45			

Ser	Gly	Ile	Gly	Thr	Gly	Gly	Ala	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
							50		55			60			

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
							65		70		75		80		

Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
							85		90			95			

Arg	Gly	Arg	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
							100		105			110			

Val	Ser	Ser													
							115								

<210> 45

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 45

gag	gtt	cag	ttg	gtg	gag	tct	ggg	gga	ggc	ttg	gta	cag	cct	ggg	ggg
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1															48
							5		10			15			

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	aga	aat
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn
20															96
								25				30			

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	
<210> 46	
<211> 115	
<212> PRT	
<213> Artificial	
<220>	
<223> Synthetic Construct	
<400> 46	
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

Val Ser Ser
115

<210> 47
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 47
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca 345
Val Ser Ser
115

<210> 48
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 49
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 49
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> 50
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

Val Ser Ser
 115

<210> 51
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 51	48
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg	
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> 52
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 52

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 53
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 53
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 54
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 55
 <211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 55

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

96

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

144

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

240

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

288

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

336

gtc tcc tca
 Val Ser Ser
 115

345

<210> 56

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 56

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 57
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1) .. (345)

<400> 57
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 58
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 59
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)...(345)

<400> 59

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

96

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

144

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

240

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

288

aga ggg agg tac tgg tac ccg tgg ggc cag gga acc ctg gtc acc
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

336

gtc tcc tca
 Val Ser Ser
 115

345

<210> 60

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 60

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 61
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)...(345)

<400> 61
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 62
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 62

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 63
 <211> 109
 <212> PRT
 <213> Artificial

<220>
 <223> 27A1 light chain variable region

<400> 63

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 64
 <211> 116
 <212> PRT
 <213> Artificial

<220>
 <223> 27A1 heavy chain variable region

<400> 64

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 65
<211> 107
<212> PRT
<213> Artificial

<220>
<223> 5A1 light chain variable region

<400> 65

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 66
<211> 123
<212> PRT
<213> Artificial

<220>
<223> 5A1 heavy chain variable region

<400> 66

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe
20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 67
<211> 107
<212> PRT
<213> Artificial

<220>
<223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp
20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 68
<211> 117
<212> PRT
<213> Artificial

<220>
<223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys
85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 69
<211> 107
<212> PRT
<213> Artificial

<220>
<223> 1B7 light chain variable region

<400> 69

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ile Ala Ser Ile Leu⁵⁰ Gln Arg Gly Val Pro Ser Arg Phe Ser Gly⁵⁵ 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 70
<211> 36
<212> DNA
<213> Artificial
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<220>
<223> Primers

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<220>
<221> misc_feature
<222> (21)..(21)
<223> N is A or G
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<220>
<221> misc_feature
<222> (24)..(24)
<223> N is G or T
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<400> 70
gtcgacgccc ccaccatgga nttnnnnnctg agcttgg

36

<210> 71
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 71
cttgaccagg cagcccaggg c

21

<210> 72
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 72
atcaaacgta cggggctgc accatctgtc ttcattc

36

<210> 73
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 73
gtttaaacgc ggccgcggat cctaacaactc tccctgttg aagctcttt

49

<210> 74
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 74
gtcgacgccc ccaccatgga aaccccagcg cagcttctct tcctcctgct actctggctc

60

ccagataaccg ctagcgaaat tgtgttgacg cagtctcca

99

<210> 75
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 75
tggagactgc gtcaacacaa ttgcgttagc ggtatctggg agccagagta gcaggaggaa
gagaagctgc gctgggttt ccatggtggc ggcgtcgac

60

99

<210> 76
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 76

atggggtcaa ccgccatcct tggcctcctc ctggctgttc tccaaggagt cgctagc

57

<210> 77

<211> 327

<212> PRT

<213> Homo sapiens

<400> 77

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1				5				10					15		

Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
		20						25					30		

Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
35					40					45					

Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
50						55				60					

Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr
65					70				75				80		

Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
				85				90				95			

Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro
			100				105				110				

Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
		115				120					125				

Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
		130				135				140					

Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp
145					150				155				160		

Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe
				165				170				175			

Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
				180				185				190			

Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu
				195			200				205				

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325